RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/828,995_

Source: _OIPE_

Date Processed by STIC: _4/30/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _O9/828,995_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of "Artificial" (NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence. . . . .

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

OIPE.

RAW SEQUENCE LISTING   DATE: 04/30/2001
PATENT APPLICATION: US/09/828,995   TIME: 09:06:25

Input Set : A:\A1-71.app   **Does Not Comply**
Output Set: N:\CRF3\04302001\I828995.raw **Corrected Diskette Needed**

```
   3 <110> APPLICANT: McCall, Catherine A.
   4         Tang, Liang
   5         Heska Corporation
   7 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND
   8         CANINE IL-13 RECEPTORS
  10 <130> FILE REFERENCE: AL-7
  12 <140> CURRENT APPLICATION NUMBER: US/09/828,995
  13 <141> CURRENT FILING DATE: 2001-04-09
  15 <150> PRIOR APPLICATION NUMBER: 60/195,659
  16 <151> PRIOR FILING DATE: 2000-04-07
  18 <150> PRIOR APPLICATION NUMBER: 60/195,874
  19 <151> PRIOR FILING DATE: 2000-04-07
  21 <160> NUMBER OF SEQ ID NOS: 104
  23 <170> SOFTWARE: PatentIn Ver. 2.1
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ERRORED SEQUENCES

```
2874 <210> SEQ ID NO: 59
2875 <211> LENGTH: 878
2876 <212> TYPE: DNA
2877 <213> ORGANISM: Canis familiaris
2879 <400> SEQUENCE: 59
2880 tttttttttt tttttctttt taaaatatga tttattcaat atttgaggaa aagcttcagt 60
2881 ttaataagac tcatatttaa catctggcca taagactgaa agttactgag tcaacagaat 120
2882 gtgtcttgat gagaaaagac ttcttttttt gtatgaaaga tcgttttcag taaagccctt 180
2883 tgcttataca aaagcaggca agttattacc aaaacaaata ttgagacaaa agcaaatggt 240
2884 atcaagaaaa atactaaggt ttccttccat atgtcacctt ccagcattg ttcatcactc 300
2885 cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag 360
2886 cataattttt ggctttcatt tgatgttctt gtgatttgta tctcattctc aactgtggta 420
2887 gtcacccaag tagtaccatc ctctgtgaat tcaatttcat aaatgaaaca tttggctgga 480
2888 atgggtcctt taggcatgtt ccatttcagg ttaatttcct ctgaattctt cacagtaaga 540
2889 ctaaggtagt ctggtggcat aggtttaact atattttgaa gctgaaaaat aaaatagctg 600
2890 ggtctgatag gctgggattc tgatgaccca ttaacacaga tgtagaaatc tttatagtct 660
2891 gatgactcca aataggaaa cctgcatccc atatttttc cattaacctt gatgtaatca 720
2892 gtacactctg ctgaatggtc caagccctca taccagtaaa acaactggta attggtatca 780
2893 aaatggacac ccatgccagg tttccaagag cagactaaat attgccagtt gtaatataca 840
2894 cagtccatat cttgaatttt agtttcccga tttccttg                        878
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 04/30/2001
PATENT APPLICATION: US/09/828,995   TIME: 09:06:27

Input Set : **A:\A1-71.app**
Output Set: **N:\CRF3\04302001\I828995.raw**

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:956 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:956 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1386 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:1386 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:1386 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1389 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:1389 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:1389 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1422 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:1422 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1534 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:1534 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:1534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1535 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:1535 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:1535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:2204 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:40
L:2204 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:40
L:2204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:2314 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48
L:2314 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:2314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:2814 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:2880 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:59
L:3016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:3114 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:62
L:3114 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:62
L:3114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:4829 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:83
L:4829 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:83
L:4829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83
L:4845 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:84
L:4845 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:84
L:4845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84
L:4861 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:85
L:4861 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:85
L:4861 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85
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VERIFICATION SUMMARY   DATE: 04/30/2001
PATENT APPLICATION: **US/09/828,995**   TIME: 09:06:27

Input Set : **A:\Al-71.app**
Output Set: **N:\CRF3\04302001\I828995.raw**

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L:4877 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:86
L:4877 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:86
L:4877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86
L:4893 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:87
L:4893 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:87
L:4893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87
L:4909 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:88
L:4909 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:88
L:4909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88
```